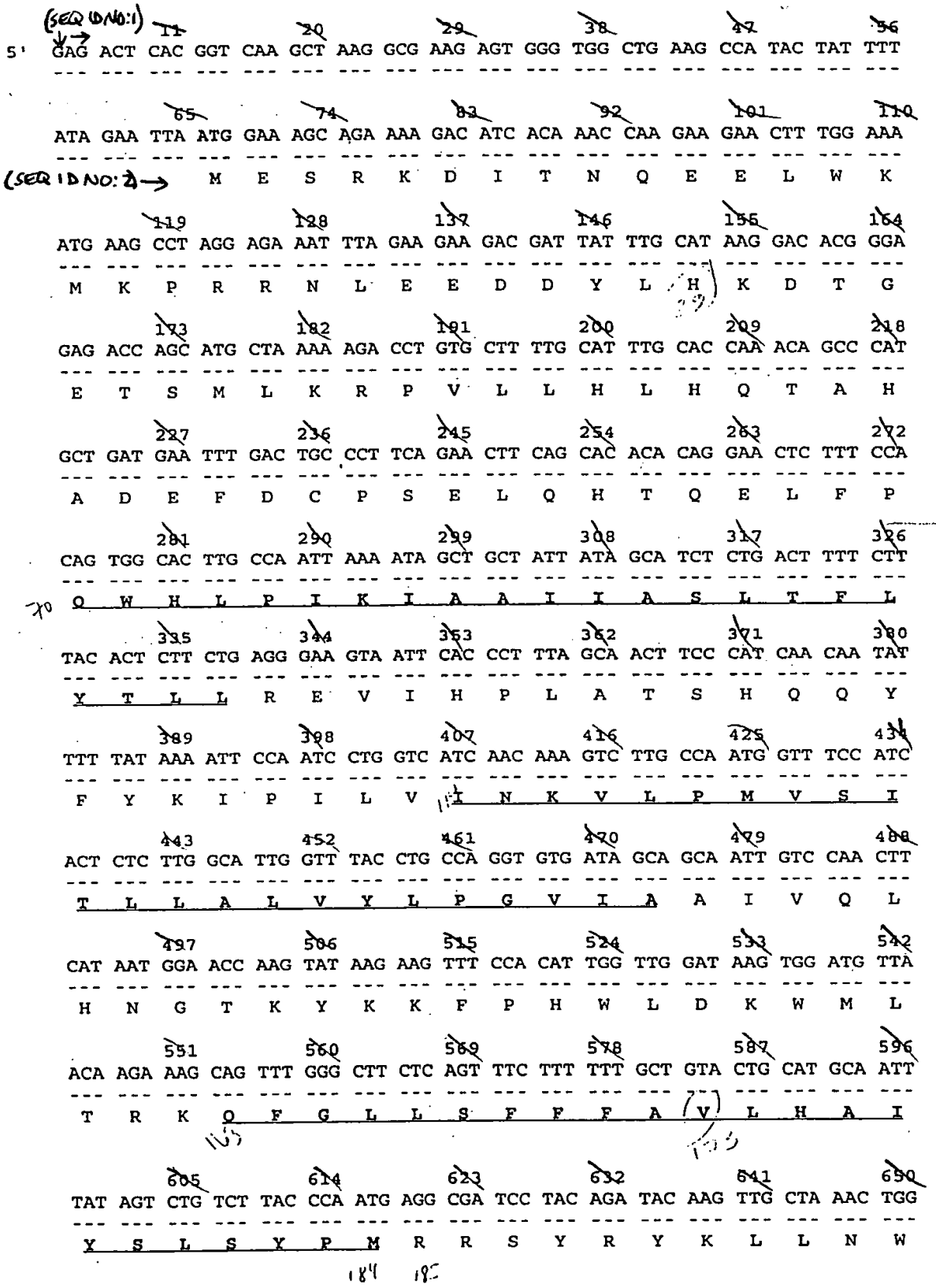
FIG. 1A


(SEQ ID NO:1)
5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT
ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA
(SEQ ID NO:2) M E S R K D I T N Q E E L W K
ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA
M K P R R N L E E D D Y L H K D T G
GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT
E T S M L K R P V L L H L H Q T A H
GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA
A D E F D C P S E L Q H T Q E L F P
CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT
Q W H L P I K I A A I I A S L T F L
TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT
Y T L L R E V I H P L A T S H Q Q Y
TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC
F Y K I P I L V I N K V L P M V S I
ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT
T L L A L V Y L P G V I A A I V Q L
CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA
H N G T K Y K K F P H W L D K W M L
ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT
T R K Q F G L L S F F F A V L H A I
TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG
Y S L S Y P M R R S Y R Y K L L N W

```
          659        668        677        686        695        704
GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   Q   Q   V   Q   Q   N   K   E   D   A   W   I   E   H   D   V

          713        722        731        740        749        758
TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   R   M   E   I   Y   V   S   L   G   I   V   G   L   A   I   L   A

          767        776        785        794        803        812
CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   L   A   V   T   S   I   P   S   V   S   D   S   L   T   W   R   E

          821        830        839        848        857        866
TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   H   Y   I   Q   S   K   L   G   I   V   S   L   L   L   G   T   I

          875        884        893        902        911        920
CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   A   L   I   F   A   W   N   K   W   I   D   I   K   Q   F   V   W

          929        938        947        956        965        974
TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   T   P   P   T   F   M   I   A   V   F   L   P   I   V   V   L   I

          983        992       1001       1010       1019       1028
TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   K   S   I   L   F   L   P   C   L   R   K   K   I   L   K   I   R

         1037       1046       1055       1064       1073       1082
CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   G   W   E   D   V   T   K   I   N   K   T   E   I   C   S   Q   L

         1091       1100       1109       1118       1127       1136
TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 *   N   Y   C   L   H   T   F   L   F   N   I   D   I   F   Y   H   Q

         1145       1154       1163       1172       1181       1190
CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   F   K   F   V   F   V   N   K   M   I   I   Q   G   K   K   K   K


AAA AA 3'
--- --
 K
```

FIG. 1B

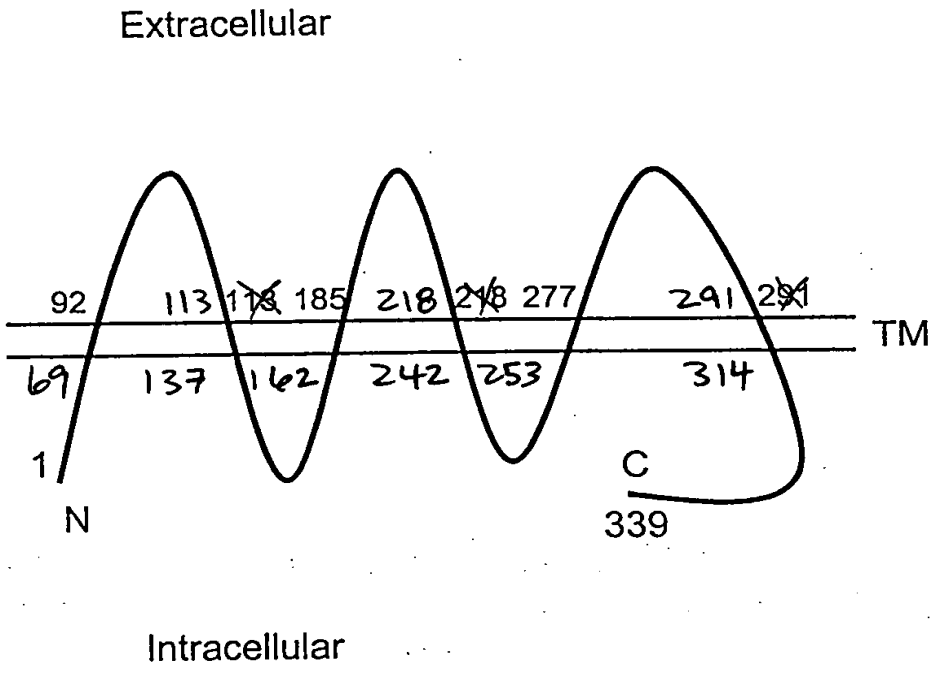

Extracellular
92
113
185
218
277
291
TM
69
137
162
242
253
314
1
N
C
339
Intracellular

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO: 3)

FIG. 4-1

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC

ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG

AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC

ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA

GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT

CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG

TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA

GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT

GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT

ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT

GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG

AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT

ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT

AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAAGGCAT

TAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTTGTTTGTTTTTTTTGAGATGAAGTCTCG

CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC

TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA

GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC

AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT

GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC

TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA

TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT

ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT

GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT

CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC

CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAG

CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA

TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

FIG. 4-2

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACT

AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA

ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT

GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT

TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA

ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATC

AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA

CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT

TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT

GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG

GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG

TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG

TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG

ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA

ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG

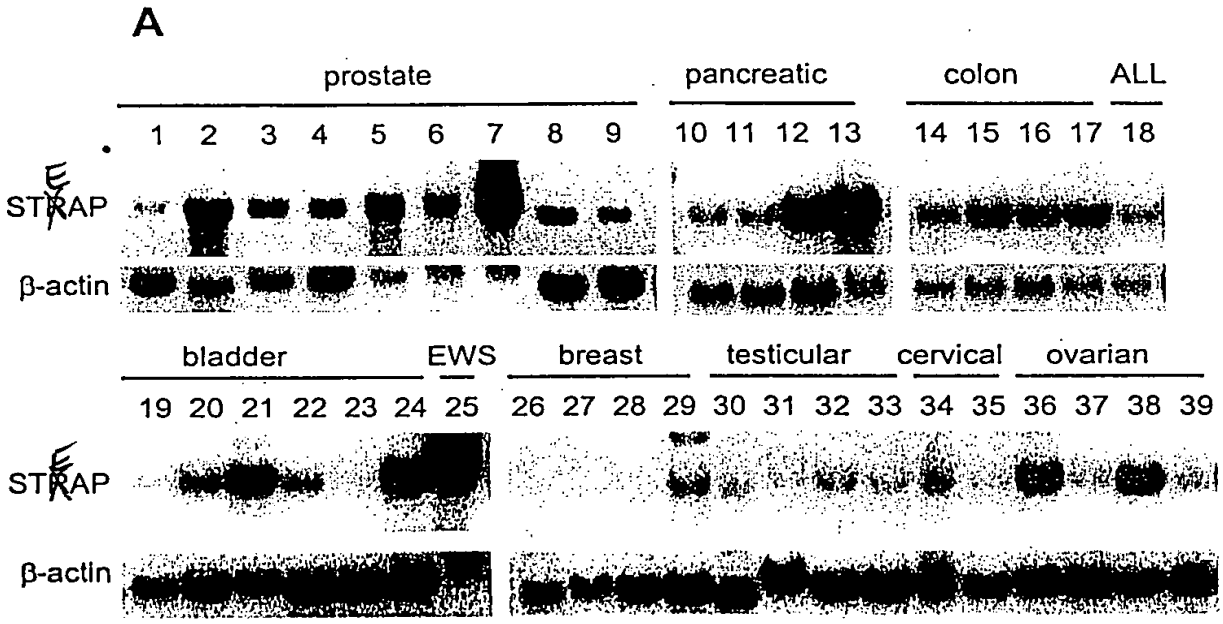
TATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT

CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAG

ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA

AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)

FIG. 5


A
prostate
pancreatic
colon
ALL
1 2 3 4 5 6 7 8 9
10 11 12 13
14 15 16 17 18
STEAP
β-actin
bladder
EWS
breast
testicular
cervical
ovarian
19 20 21 22 23 24 25
26 27 28 29 30 31 32 33 34 35 36 37 38 39
STEAP
β-actin

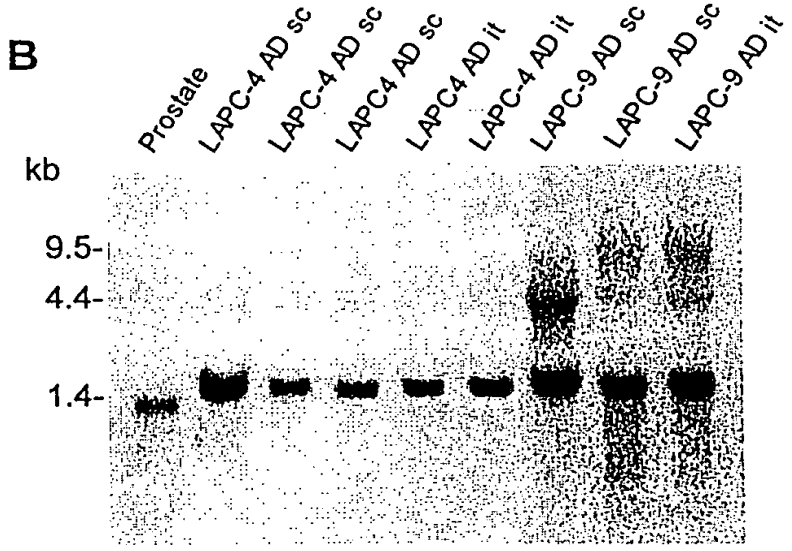

B
Prostate
LAPC-4 AD sc
LAPC-4 AD sc
LAPC4 AD sc
LAPC4 AD it
LAPC-4 AD it
LAPC-9 AD sc
LAPC-9 AD sc
LAPC-9 AD it
kb
9.5-
4.4-
1.4-

FIG. 6

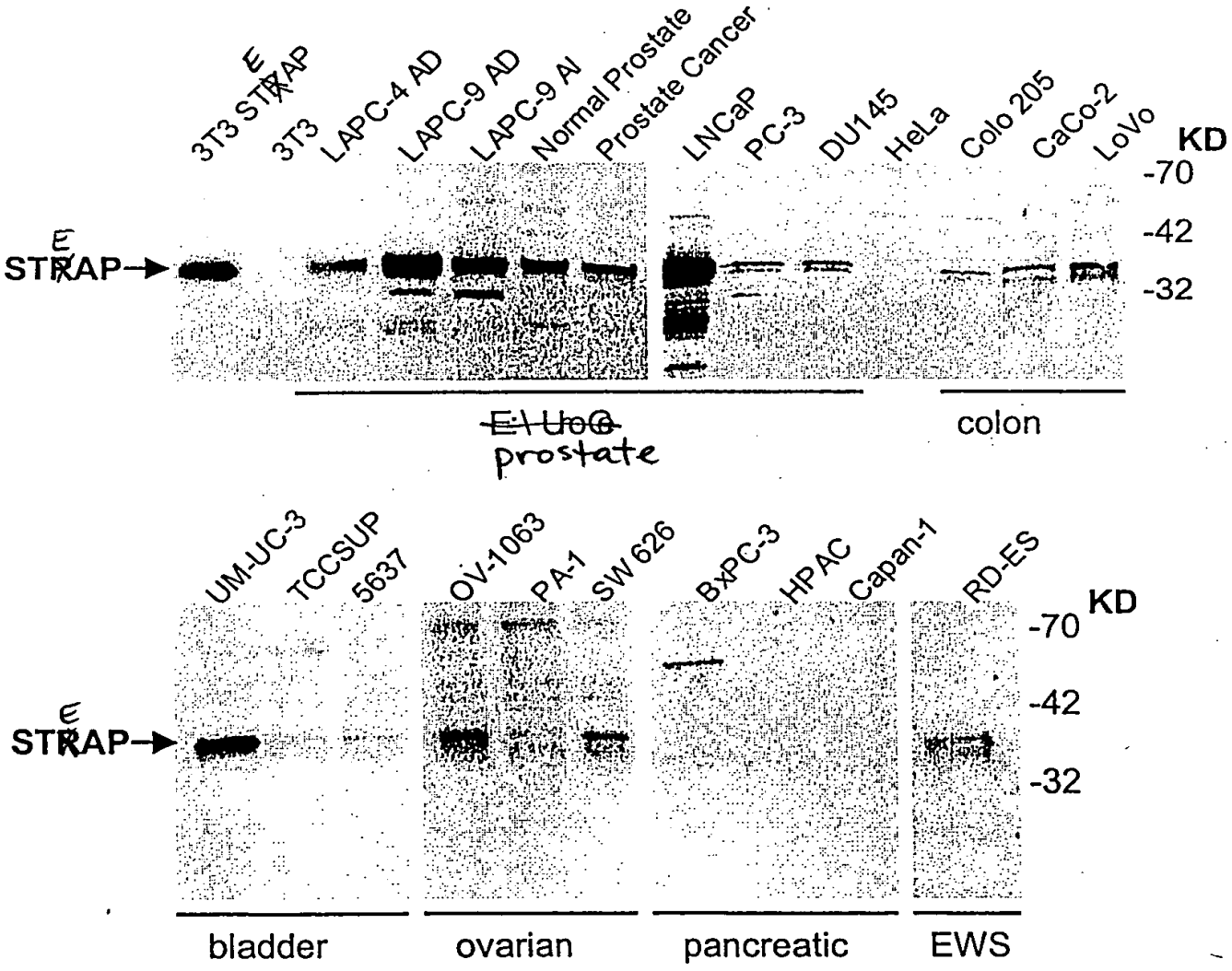

3T3 STRAP
3T3
LAPC-4 AD
LAPC-9 AD
LAPC-9 AI
Normal Prostate
Prostate Cancer
LNCaP
PC-3
DU145
HeLa
Colo 205
CaCo-2
LoVo
KD
-70
-42
-32
STRAP
prostate
colon
UM-UC-3
TCCSUP
5637
OV-1063
PA-1
SW 626
BxPC-3
HPAC
Capan-1
RD-ES
bladder
ovarian
pancreatic
EWS

FIG. 7

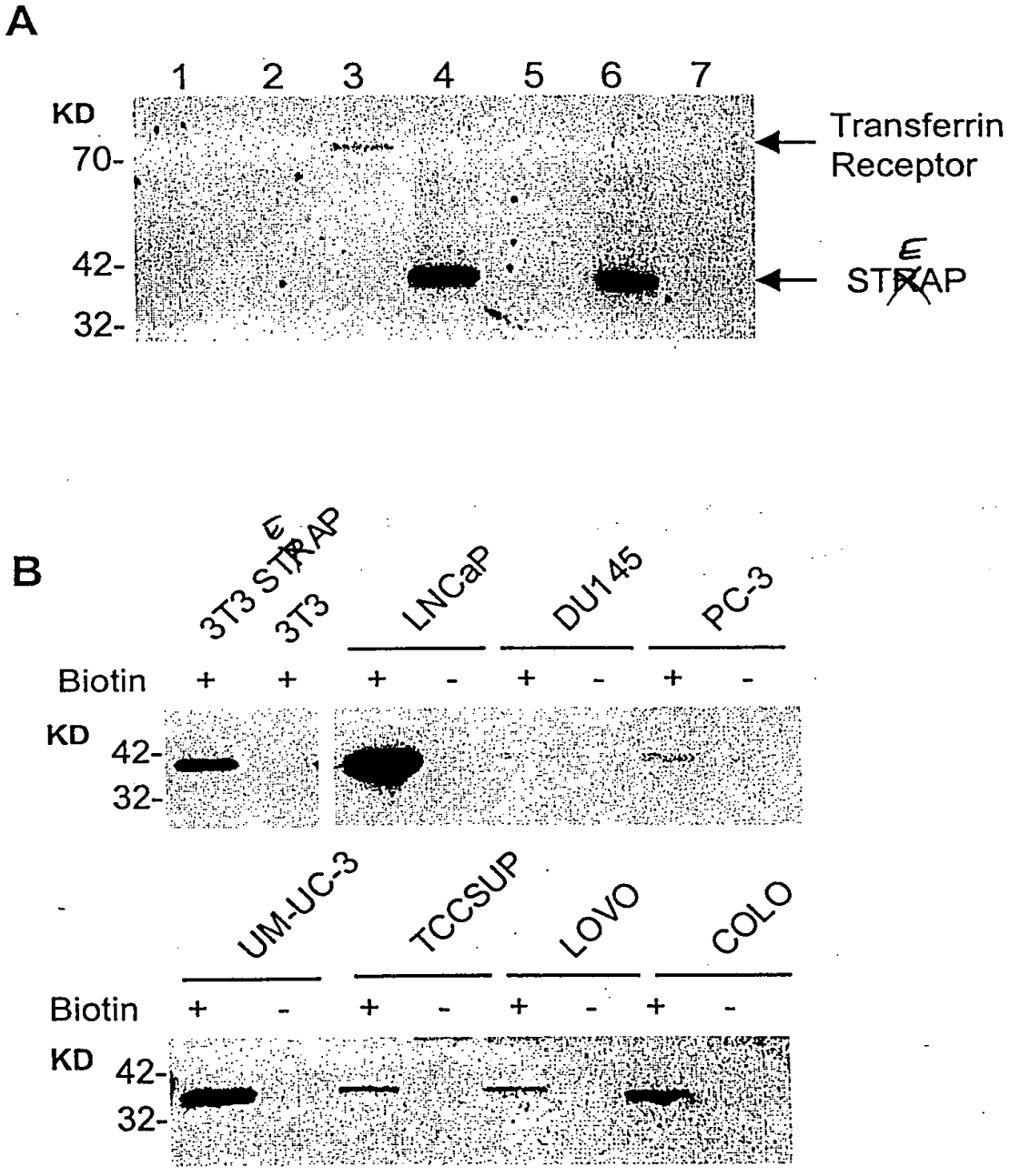

A
1 2 3 4 5 6 7
KD
70-
42-
32-
Transferrin Receptor
STEAP
B
3T3 STEAP
3T3
LNCaP
DU145
PC-3
Biotin + + + - + - + -
KD
42-
32-
UM-UC-3
TCCSUP
LOVO
COLO
Biotin + - + - + - + -
KD
42-
32-

FIG. 9

```
          10          19          28          37          46          55
5'  GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

          64          73          82          91         100         109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

         118         127         136         145         154         163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

         172         181         190         199         208         217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

         226         235         244         253         262         271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

         280         289         298         307         316         325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

         334         343         352         361         370         379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

         388         397         406         415         424         433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

         442         451         460         469         478         487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

         496         505         514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3' (SEQ ID NO: 7)
    --- --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala  (SEQ ID NO: 8)
```

FIG. 10

STEAP-2, AA508880 (NCI_CGAP Pr6)
ggtcgacttttccttttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaaacctggtta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatggtccatgttgcctacagcctctgcttaccga
tgagaaggtcagagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment
TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTACATTCCTCAGCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT (SEQ ID NO:10)

AI139607 (testis EST)
aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaatacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtccaaactgggttatttgaccctgatcttgtgtacagcccacaccctggtgtacggtgggaagagattcctc
agcccttcaaatctcagatggtatcttcctgcagcctacgtgttagggcttatcattccttgcactgtgctggtga
tcaagtttgtcctaatcatgccatgtgtagacaacacccttacaaggatccgccagggctgggaaaggaactcaaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa (SEQ ID NO:11)

R80991 (placental EST)
ggccgcggcanccgctacgacctggtcaacctggcagtcaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg
tgacctcactgccgtccattgcaaactcgctcaactggagggagttcagcttcgttcagtcctcactgggctttgt
ggccntcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctnccctcccaccttcacgntcacgctgctggtgccctgcgttcgttcatcctgggccaaagccctgtttntac
tgccttgcattcagccgnaga (SEQ ID NO:12)

FIG. 11A

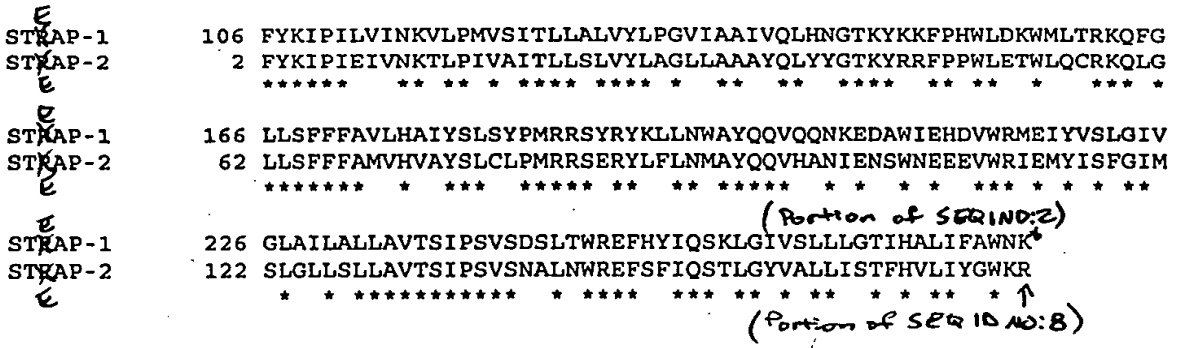
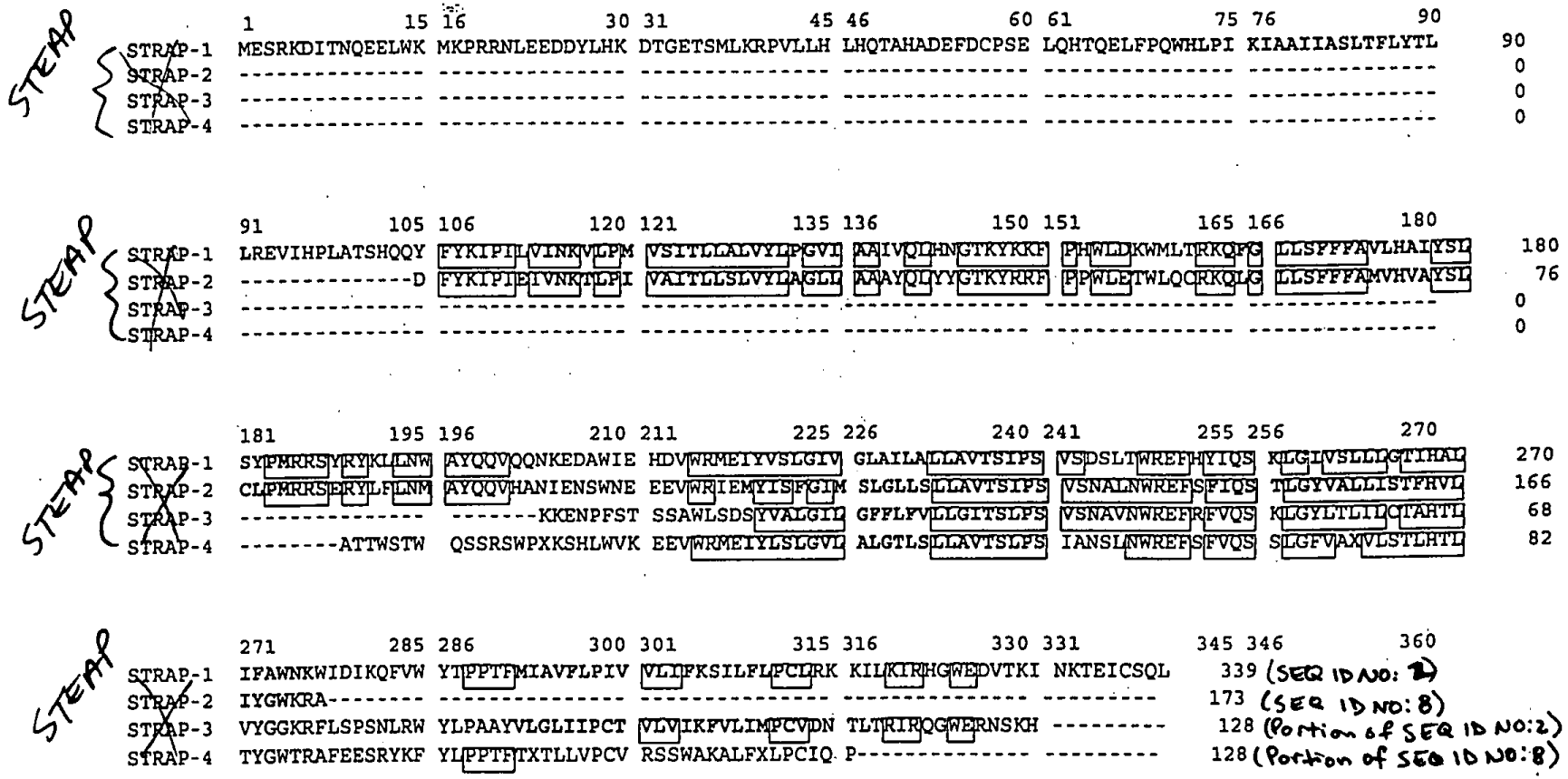

STRAP-1 106 FYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2 2 FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG
STRAP-1 166 LLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIV
STRAP-2 62 LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
(Portion of SEQ ID NO:2)
STRAP-1 226 GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
STRAP-2 122 SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
(Portion of SEQ ID NO:8)

FIG. 11B


STEAP
STRAP-1
STRAP-2
STRAP-3
STRAP-4
1 15 16 30 31 45 46 60 61 75 76 90
MESRKDITNQEELWK MKPRRNLEEDDYLHK DTGETSMLKRPVLLH LHQTAHADEFDCPSE LQHTQELFPQWHLPI KIAAIIASLTFLYTL 90
0
0
0
91 105 106 120 121 135 136 150 151 165 166 180
LREVIHPLATSHQQY FYKIPILVINKVLPM VSITLLALVYLPGVI AAIVQLHNGTKYKKF PHWLDKWMLTRKQFG LLSFFFAVLHAIYSL 180
-D FYKIPIEIVNKTLPI VAITLLSLVYLAGLL AAAYQLYYGTKYRRF PPWLETWLQCRKQLG LLSFFFAMVHVAYSL 76
0
0
181 195 196 210 211 225 226 240 241 255 256 270
SYPMRRSYRYKLLNW AYQQVQQNKEDAWIE HDVWRMEIYVSLGIV GLAILALLAVTSIPS VSDSLIWREFHYIQS KLGIVSLLLGTIHAL 270
CLPMRRSERYLFLNM AYQQVHANIENSWNE EEVWRIEMYISFGIM SLGLLSLLAVTSIPS VSNALNWREFSFIQS TLGYVALLISTFHVL 166
-------KKENPFST SSAWLSDSYVALGIL GFFLFVLLGITSLPS VSNAVNWREFRFVQS KLGYLTLILQTAHTL 68
--------ATTWSTW QSSRSWPXKSHLWVK EEVWRMEIYLSLGVL ALGTLSLLAVTSLPS IANSLNWREFSFVQS SLGFVAXVLSTLHTL 82
271 285 286 300 301 315 316 330 331 345 346 360
IFAWNKWIDIKQFVW YTPPTFMIAVFLPIV VLIFKSILFLPCLRK KILKIRHGWEDVTKI NKTEICSQL 339 (SEQ ID NO: 2)
IYGWKRA 173 (SEQ ID NO: 8)
VYGGKRFLSPSNLRW YLPAAYVLGLIIPCT VLVIKFVLIMPCVDN TLTRIRQGWERNSKH 128 (Portion of SEQ ID NO:2)
TYGWTRAFEESRYKF YLPPTFTXTLLVPCV RSSWAKALFXLPCIQ P 128 (Portion of SEQ ID NO:8)

~~FIG.14~~

FIG. 14A

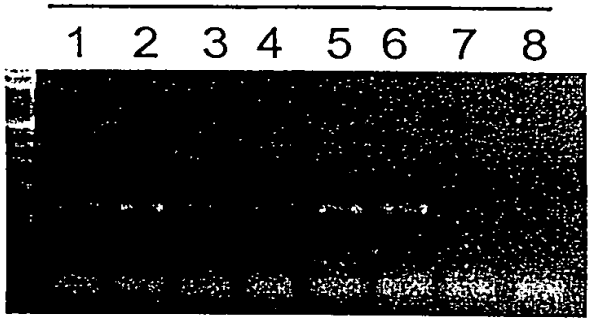
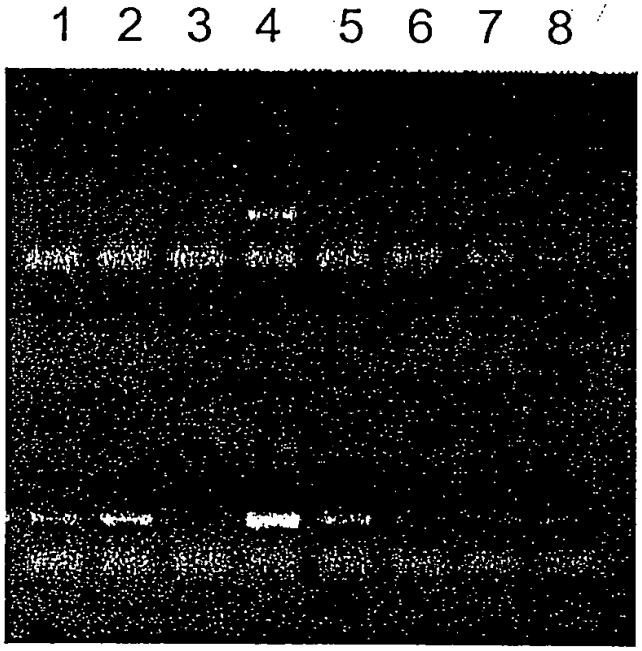


FIG. 14B



~~A~~

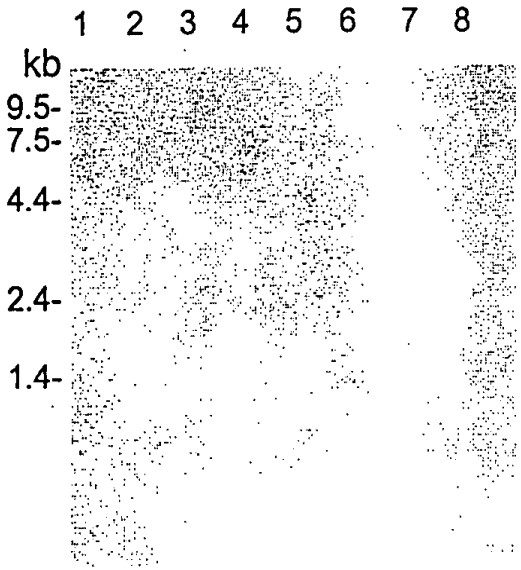
1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

~~B~~

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

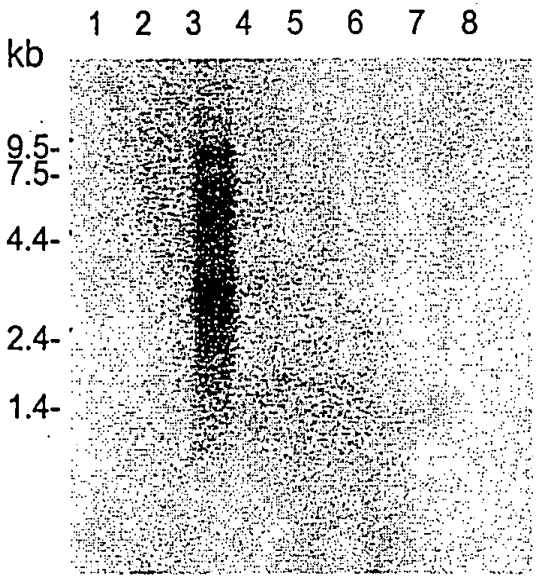
FIG. 15

FIG. 15A



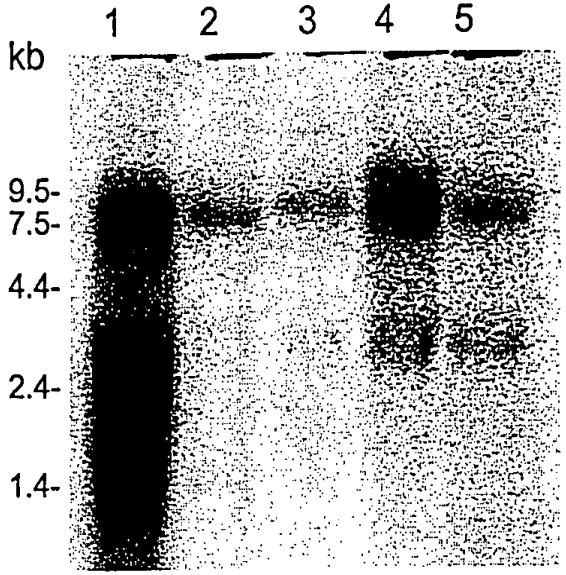
A
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

FIG. 15B



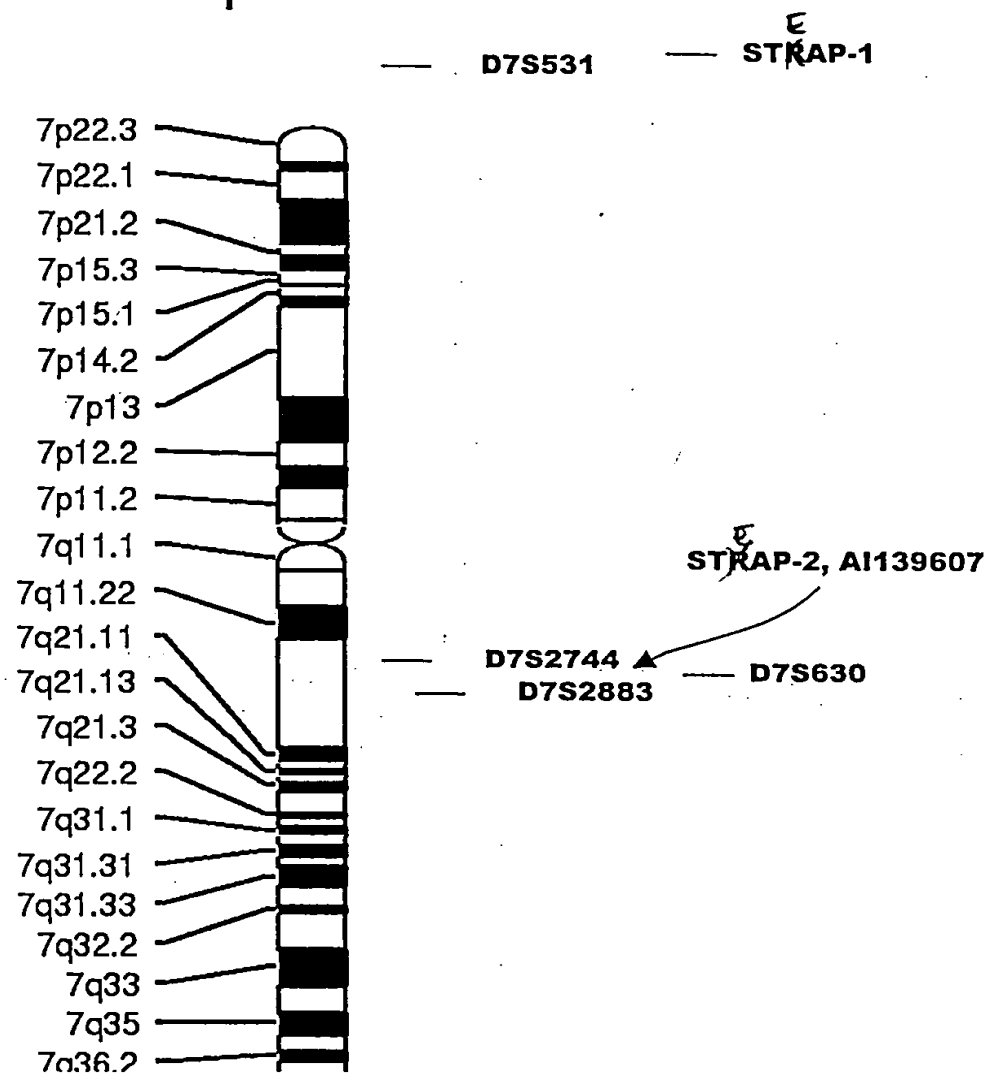
B
1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



C
1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 17


GDB Compreher
D7S531
STRAP-1
7p22.3
7p22.1
7p21.2
7p15.3
7p15.1
7p14.2
7p13
7p12.2
7p11.2
7q11.1
7q11.22
7q21.11
7q21.13
7q21.3
7q22.2
7q31.1
7q31.31
7q31.33
7q32.2
7q33
7q35
7q36.2
STRAP-2, AI139607
D7S2744
D7S2883
D7S630